

Patent Application US/07/599,543C

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Opperman, Hermann
Ozkaynak, Engin
Rueger, David C.
Kuberasampath, Thangavel

(ii) TITLE OF INVENTION: Osteogenic Proteins

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Testa Hurwitz & Thibault

(B) STREET: 53 State Street

(C) CITY: Boston

(D) STATE: Massachusetts

(E) COUNTRY: U.S.A.

(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 720 kb storage

(B) COMPUTER: IBM XT

(C) OPERATING SYSTEM: DOS 3.30

(D) SOFTWARE: ASC II

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/599,543

(B) FILING DATE: 18-Oct-90

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 569,920

(B) FILING DATE: 20-Aug-90

(C) APPLICATION NUMBER: US 315,342

(D) FILING DATE: 23-Feb-89

(E) APPLICATION NUMBER: US 422,699

(F) FILING DATE: 17-Oct-89

#11
Does not comply
- Send a notice -

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: mOP2 (mature)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

79 Ala Ala Arg Pro Leu Lys Arg ArgGln
80 1 5 → S
81 Pro Lys Lys Thr Asn Glu Leu ProHis
82 10 15 numbering off, too
83 Pro Asn Lys Leu Pro Gly Ile PheAsp
84 20 25
85 Asp Gly His Gly Ser Arg Gly ArgGlu
86 30 35
87 Val Cys Arg Arg His Glu Leu TyrVal
88 40 45
89 Arg Phe Arg Asp Leu Gly Trp LeuAsp
90 50
91 Trp Val Ile Ala Pro Gln Gly TyrSer
92 55 60
93 Ala Tyr Tyr Cys Glu Gly Glu CysAla
94 65 70
95 Phe Pro Leu Asp Ser Cys Met AsnAla
96 75 80
97 Thr Asn His Ala Ile Leu Gln SerLeu
98 85 90
99 Val His Leu Met Lys Pro Asp ValVal
100 95
101 Pro Lys Ala Cys Cys Ala Pro ThrLys
102 100 105
103 Leu Ser Ala Thr Ser Val Leu TyrTyr
104 110 115
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space needed
to separate amino
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135 Asp Ser Ser Asn Asn Val Ile LeuArg
136 120 125
137 Lys His Arg Asn Met Val Val LysAla
138 130135
139 Cys Gly Cys His
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142 (2) INFORMATION FOR SEQ ID NO:2:
143 (i) SEQUENCE CHARACTERISTICS:
144 (A) LENGTH:1930 base pairs
145 (B) TYPE: nucleic acid
146 (C) STRANDEDNESS: single
147 (D) TOPOLOGY: linear
148 (ii) MOLECULE TYPE: cDNA
149 (iii) HYPOTHETICAL: no
150 (iv) ANTI-SENSE: no
151 (vi) ORIGINAL SOURCE:
152 (A) ORGANISM: mouse
153 (F) TISSUE TYPE: embryo
154 (ix) FEATURE:
155 (A) NAME: mop2
156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
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158 GGAATTCCGC TGCCAGGCAC AGGTGCGCCG TCTGGTCCTC 40
159 CCCGTCTGGC GTCAGCCGAG CCCGACCAGC TACCAGTGGA 80

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160 TGC GCG CCG GCT GAA AGT CCG GAG ATG GCT ATG CGT 115
161 Met Ala Met Arg
162 1
163 CCC GGG CCA CTC TGG CTA TTG GGC CTT GCT CTG 148
164 Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu
165 5 10 15
166 TGC GCG CTG GGA GGC GGC CAC GGT CCC GGT CCC 181
167 Cys Ala Leu Gly Gly Gly His Gly Pro Gly Pro
168 20 25
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200 CCG CAC ACC TGT CCC CAG CGT CGC CTG GGA GCG 214
201 Pro His Thr Cys Pro Gln Arg Arg Leu Gly Ala
202 30 35
203 CGC GAC CCG GAC ATG CAG CGT GAA ATC CTG CCG 247
204 Arg Asp Arg Asp Met Gln Arg Glu Ile Leu Pro
205 40 45
206 GTG CTC GGG CTA CCG GGA CGC CCC GAC CCC GTG 280
207 Val Leu Gly Leu Pro Gly Arg Pro Asp Pro Val
208 50 55
209 CAC AAC CCG CCG CTG CCC GGC ACG CAG CGT GCG 313
210 His Asn Pro Pro Leu Pro Gly Thr Gln Arg Ala
211 60 65 70
212 CCC CTC TTC ATG TTG GAC CTA TAC CAC GCC ATG 346

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213 Pro Leu Phe Met Leu Asp Leu Tyr His Ala Met
214 75 80
215 ACC GAT GAC GAC GAC GGC GGG CCA CCA CAG GCT 379
216 Thr Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala
217 85 90
218 CAC TTA GGC CGT GCC GAC CTG GTC ATG AGC TTC 412
219 His Leu Gly Arg Ala Asp Leu Val Met Ser Phe
220 95 100
221 GTC AAC ATG GTG GAA CGC GAC CGT ACC CTG GGC 445
222 Val Asn Met Val Glu Arg Asp Arg Thr Leu Gly
223 105 110
224 TAC CAG GAG CCA CAC TGG AAG GAA TTC CAC TTT 478
225 Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe
226 115 120 125
227 GAC CTA ACC CAG ATC CCT GCT GGC GAG GCT GTC 511
228 Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val
229 130 135
230 ACA GCT GCT GAG TTC CGG ATC TAC AAA GAA CCC 544
231 Thr Ala Ala Glu Phe Arg Ile Tyr Lys Glu Pro
232 140 145
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265 AGC ACC CAC CCG CTC AAC ACA ACC CTC CAC ATC 577

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266 Ser Thr His Pro Leu Asn Thr Thr Leu His Ile
267 150 155
268 AGC ATG TTC GAA GTG GTC CAA GAG CAC TCC AAC 610
269 Ser Met Phe Glu Val Val Gln Glu His Ser Asn
270 160 165
271 AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG 643
272 Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln
273 170 175 180
274 ACG CTC CGA TCT GGG GAC GAG GGC TGG CTG GTG 676
275 Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val
276 185 190
277 CTG GAC ATC ACA GCA GCC AGT GAC CGA TGG CTG 709
278 Leu Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu
279 195 200
280 CTG AAC CAT CAC AAG GAC CTG GGA CTC CGC CTC 742
281 Leu Asn His His Lys Asp Leu Gly Leu Arg Leu
282 205 210
283 TAT GTG GAA ACC GCG GAT GGG CAC AGC ATG GAT 775
284 Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp
285 215 220
286 CCT GGC CTG GCT GGT CTG CTT GGA CGA CAA GCA 808
287 Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala
288 225 230 235
289 CCA CGC TCC AGA CAG CCT TTC ATG GTA ACC TTC 841
290 Pro Arg Ser Arg Gln Pro Phe Met Val Thr Phe
291 240 245
292 TTC AGG GCC AGC CAG AGT CCT GTG CGG GCC CCT 874
293 Phe Arg Ala Ser Gln Ser Pro Val Arg Ala Pro
294 250 255
295 CGG GCA GCG AGA CCA CTG AAG AGG AGG CAG CCA 907
296 Arg Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro
297 260 265
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330 AAG AAA ACG AAC GAG CTT CCG CAC CCC AAC AAA 940
331 Lys Lys Thr Asn Glu Leu Pro His Pro Asn Lys
332 270 275
333 CTC CCA GGG ATC TTT GAT GAT GGC CAC GGT TCC 973
334 Leu Pro Gly Ile Phe Asp Asp Gly His Gly Ser
335 280 285 290
336 CGC GGC AGA GAG GTT TGC CGC AGG CAT GAG CTC 1006
337 Arg Gly Arg Glu Val Cys Arg Arg His Glu Leu
338 295 300
339 TAC GTC AGA TTC CGT GAC CTT GGC TGG CTG GAC 1039
340 Tyr Val Arg Phe Arg Asp Leu Gly Trp Leu Asp
341 305 310
342 TGG GTC ATC GCC CCC CAG GGC TAC TCT GCC TAT 1072
343 Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr
344 315 320
345 TAC TGT GAG GGG GAG TGT GCT TTC CCA CTG GAC 1105
346 Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asp
347 325 330
348 TCC TGT ATG AAC GCC ACC AAC CAT GCC ATC TTG 1138
349 Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu
350 335 340 345
351 CAG TCT CTG GTG CAC CTG ATG AAG CCA GAT GTT 1171
352 Gln Ser Leu Val His Leu Met Lys Pro Asp Val
353 350 355
354 GTC CCC AAG GCA TGC TGT GCA CCC ACC AAA CTG 1204
355 Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu
356 360 365
357 AGT GCC ACC TCT GTG CTG TAC TAT GAC AGC AGC 1237
358 Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser
359 370 375
360 AAC AAT GTC ATC CTG CGT AAA CAC CGT AAC ATG 1270
361 Asn Asn Val Ile Leu Arg Lys His Arg Asn Met
362 380 385
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395 GTG GTC AAG GCC TGT GGC TGC CAC 1294
396 Val Val Lys Ala Cys Gly Cys His
397 390 400
398 TGAGGCCCGG CCCAGCATCC TGCTTCTACT ACCTTACCAT 1334
399 CTGGCCGGGC CCCTCTCCAG AGGCAGAAAC CCTTCTATGT 1374
400 TATCATAGCT CAGACAGGGG CAATGGGAGG CCCTTCACTT 1414
401 CCCCTGGCCA CTTCTGTCTA AAATTCTGGT CTTTCCCAGT 1454
402 TCCTCTGTCC TTCATGGGGT TTCGGGGCTA TCACCCCGCC 1494
403 CTCTCCATCC TCCTACCCCA AGCATAGACT GAATGCACAC 1534
404 AGCATCCCAG AGCTATGCTA ACTGAGAGGT CTGGGGTCAG 1574
405 CACTGAAGGC CCACATGAGG AAGACTGATC CTTGGCCATC 1614
406 CTCAGCCAC AATGGCAAAT TCTGGATGGT CTAAGAAGCC 1654
407 CTGGAATTCT AAAC TAGATG ATCTGGGCTC TCTGCACCAT 1694
408 TCATTGTGGC AGTTGGGACA TTTT TAGGTA TAACAGACAC 1734
409 ATACACTTAG ATCAATGCAT CGCTGTACTC CTTGAAATCA 1774
410 GAGCTAGCTT GTTAGAAAA GAATCAGAGC CAGGTATAGC 1814
411 GGTGCATGTC ATTAATCCCA GCGCTAAAGA GACAGAGACA 1854
412 GGAGAATCTC TGTGAGTTCA AGGCCACATA GAAAGAGCCT 1894
413 GTCTCGGGAG CAGGAAAAA AAAAAAACG GAATTC 1930

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416 (2) INFORMATION FOR SEQ ID NO:3:
417 (i) SEQUENCE CHARACTERISTICS:
418 (A) LENGTH:139 amino acids
419 (B) TYPE: amino acid
420 (D) TOPOLOGY: linear
421 (ii) MOLECULE TYPE: protein
422 (ix) FEATURE:
423 (A) NAME: hOP2 (mature)
424 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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426	Ala	Val	Arg	Pro	Leu	Arg	Arg	ArgGln
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428	Pro	Lys	Lys	Ser	Asn	Glu	Leu	ProGln
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462	Ala	Asn	Arg	Leu	Pro	Gly	Ile	PheAsp
463		20		25				
464	Asp	Val	His	Gly	Ser	His	Gly	ArgGln
465	30		35					
466	Val	Cys	Arg	Arg	His	Glu	Leu	TyrVal
467	40	45						
468	Ser	Phe	Gln	Asp	Leu	Gly	Trp	LeuAsp
469		50						
470	Trp	Val	Ile	Ala	Pro	Gln	Gly	TyrSer
471	55	60						
472	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	CysSer
473		65		70				
474	Phe	Pro	Leu	Asp	Ser	Cys	Met	AsnAla
475	75	80						
476	Thr	Asn	His	Ala	Ile	Leu	Gln	SerLeu
477	85	90						

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478 Val His Leu Met Lys Pro Asn AlaVal
479 95
480 Pro Lys Ala Cys Cys Ala Pro ThrLys
481 100 105
482 Leu Ser Ala Thr Ser Val Leu TyrTyr
483 110 115
484 Asp Ser Ser Asn Asn Val Ile LeuArg
485 120 125
486 Lys Ala Arg Asn Met Val Val LysAla
487 130135
488 Cys Gly Cys His
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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1941 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

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531 (vi) ORIGINAL SOURCE:
532 (A) ORGANISM: homo sapiens
533 (F) TISSUE TYPE: hippocampus
534 (ix) FEATURE:
535 (A) NAME: hOP2
536 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
537
538 GGAATTCCGG CCACAGTGGC GCCGGCAGAG CAGGAGTGGC 40
539 TGGAGGAGCT GTGGTTGGAG CAGGAGGTGG CACGGCAGGG 80
540 CTGGAGGGCT CCCTATGAGT GCGGAGACG GCCCAGGAGG 120
541 CGCTGGAGCA ACAGCTCCCA CACCGCACCA AGCGGTGGCT 160
542 GCAGGAGCTC GCCCATCGCC CCTGCGCTGC TCGGACCGCG 200
543 GCCACAGCCG GACTGGCGGG TACGGCGGCG ACAGAGGCAT 240
544 TGGCCGAGAG TCCCAGTCCG CAGAGTAGCC CCGGCCTCGA 280
545 GCGGGTGGCG TCCCAGTCCG CTCCGTCCAG GAGCCAGGAC 320
546 AGGTGTGCGC CGGCGGGGCT CCAGGGACCG CGCCTGAGGC 360
547 CGGCTGCCCC CGCGTCCCCG CCCGCCCCGC CGCCCGCCGC 400
548 CCGCCGAGCC CAGCCTCCTT GCCGTGCGGG CGTCCCCAGG 440
549 CCCTGGGTCTG GCCGCGGAGC CGATGCGCGC CCGCTGAGCG 480
550 CCCCAGCTGA GCGCCCCCGG CCTGCC ATG ACC GCG CTC 518
551 Met Thr Ala Leu
552 1
553 CCC GGC CCG CTC TGG CTC CTG GGC CTG GCG CTA 551
554 Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu
555 5 10 15
556 TGC GCG CTG GGC GGG GGC GGC CCC GGC CTG CGA 584
557 Cys Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg
558 20 25
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592 CCC CCG CCC GGC TGT CCC CAG CGA CGT CTG GGC 617
593 Pro Pro Pro Gly Cys Pro Gly arg Arg Leu Gly
594 30 35
595 GCG CGC GAC CGG GAC GTG CAG CGC GAG ATC CTG 650
596 Ala Arg Asp Arg Asp Val Gln Arg Glu Ile Leu
597 40 45
598 GCG GTG CTC GGG CTG CCT GGG CGG CCC CGG CCC 683
599 Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro
600 50 55
601 CGC GCG CCA CCC GCC GCC TCC CGG CTG CCC GCG 716
602 Arg Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala
603 60 65 70
604 TCC GCG CCG CTC TTC ATG CTG GAC CTG TAC CAC 749
605 Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His
606 75 80
607 CGC ATG GCC GGC GAC GAC GAC GAG GAC GGC GCC 782
608 Arg Met Ala Gly Asp Asp Asp Glu Asp Gly Ala
609 85 90
610 GCG GAG GCC CTG GGC CGC GCC GAC CTG GTC ATG 815
611 Ala Glu Ala Leu Gly Arg Ala Asp Leu Val Met
612 95 100
613 AGC TTC GTT AAC ATG GTG GAG CGA GAC CGT GCC 848
614 Ser Phe Val Asn Met Val Glu Arg Asp Arg Ala
615 105 110
616 CTG GGC CAC CAG GAG CCC CAT TGG AAG GAG TTC 881
617 Leu Gly His Gln Glu Pro His Trp Lys Glu Phe
618 115 120 125
619 CGC TTT GAC CTG ACC CAG ATC CCG GCT GGG GAG 914
620 Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu
621 130 135
622 GCG GTC ACA GCT GCG GAG TTC CGG ATT TAC AAG 947
623 Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys
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657 GTG CCC AGC ATC CAC CTG CTC AAC AGG ACC CTC 980
658 Val Pro Ser Ile His Leu Leu Asn Arg Thr Leu
659 150 155
660 CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG 1013
661 His Val Ser Met Phe Gln Val Val Gln Glu Gln
662 160 165
663 TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT 1046
664 Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp
665 170 175 180
666 CTT CAG ACG CTC CGA GCT GGA GAC GAG GGC TGG 1079
667 Leu Gln Thr Leu Arg Ala Gly Asp Glu Gly Trp
668 185 190
669 CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC 1112
670 Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys
671 195 200
672 TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA CTC 1145
673 Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu
674 205 210
675 CGC CTC TAT GTG GAG ACT GAG GAC GGG CAC AGC 1178
676 Arg Leu Tyr Val Glu Thr Glu Asp Gly His Ser
677 215 220
678 GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT CAA 1211
679 Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln
680 225 230 235
681 CGG GCC CCA CGC TCC CAA CAG CCT TTC GTG GTC 1244
682 Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val
683 240 245
684 ACT TTC TTC AGG GCC AGT CCG AGT CCC ATC CGC 1277
685 Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg
686 250 255
687 ACC CCT CGG GCA GTG AGG CCA CTG AGG AGG AGG 1310
688 Thr Pro Arg Ala Val Arg Pro Leu Arg Arg Arg
689 260 265

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722 CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG GCC 1343
723 Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala
724 270 275
725 AAC CGA CTC CCA GGG ATC TTT GAT GAC GTC CAC 1376
726 Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His
727 280 285 290
728 GGC TCC CAC GGC CGG CAG GTC TGC CGT CGG CAC 1409
729 Gly Ser His Gly Arg Gln Val Cys Arg Arg His
730 295 300
731 GAG CTC TAC GTC AGC TTC CAG GAC CTC GGC TGG 1442
732 Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp
733 305 310
734 CTG GAC TGG GTC ATC GCT CCC CAA GGC TAC TCG 1475
735 Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser
736 315 320
737 GCC TAT TAC TGT GAG GGG GAG TGC TCC TTC CCA 1508
738 Ala Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro
739 325 330
740 CTG GAC TCC TGC ATG AAT GCC ACC AAC CAC GCC 1541
741 Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala
742 335 340 345

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743 ATC CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA 1574
744 Ile Leu Gln Ser Leu Val His Leu Met Lys Pro
745 350 355
746 AAC GCA GTC CCC AAG GCG TGC TGT GCA CCC ACC 1607
747 Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr
748 360 365
749 AAG CTG AGC GCC ACC TCT GTG CTC TAC TAT GAC 1640
750 Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp
751 370 375
752 AGC AGC AAC AAC GTC ATC CTG CGC AAA GCC CGC 1673
753 Ser Ser Asn Asn Val Ile Leu Arg Lys Ala Arg
754 380 385
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787 AAC ATG GTG GTC AAG GCC TGC GGC TGC CAC 1703
788 Asn Met Val Val Lys Ala Cys Gly Cys His
789 390 395
790 TGAGTCAGCC CGCCCAGCCC TACTGCAGCA ATTCAGTGGC 1743
791 CGTCGTTTTA CAACGTGTGA CTGGGAAAAC CCTGGCGTTA 1783
792 CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG 1823
793 CTGGCTAATA GCGAAGAGGC CCCGCACCGA TCGCCCTTCC 1863
794 CAACAGTTGC GCCCCAGTGA ATGGCGAATG GCAAATTGTA 1903
795 AGCGTTAATA TTTTGTTAAA ATTCGCGTTA AATTTTTT 1941

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798 (2) INFORMATION FOR SEQ ID NO:5:
799 (i) SEQUENCE CHARACTERISTICS:
800 (A) LENGTH:98 amino acids
801 (B) TYPE: amino acid
802 (D) TOPOLOGY: linear
803 (ii) MOLECULE TYPE: protein
804 (ix) FEATURE:
805 (D) OTHER INFORMATION: wherein "res."
806 means "residue" and Xaa at res. 2 = (Lys or Arg); Xaa at
807 res.3 = (Lys or Arg); Xaa res.9 = (Ser or Arg); Xaa at
808 res.11 = (Arg or Gln); Xaa at res.16 = (Gln or Leu); Xaa
809 at res. 19 = (Ile or Val); Xaa at res.23 = (Glu or Gln);
810 Xaa at res.26 = (Ala or Ser); Xaa at res. 34 = (Ala or
811 or Ser); Xaa at res.38= (Asn or Asp); Xaa at res. 40 =
812 (Tyr or Cys); Xaa at res.49 = (Val or Leu); Xaa at
813 res.52= (His or Asn); Xaa at res. 53 = (Phe or
814 Leu); Xaa at res. 54 = (Ile or Met); Xaa at res. 55 = (Asn
815 or Lys); Xaa at res. 56 = (Glu, Asp or Asn); Xaa at res.
816 57=(Thr, Ala or Val); Xaa at res. 61 = (Pro or Ala);
817 Xaa at res. 67=(gln or Lys); Xaa at res. 69 =
818 (Asn or Ser); Xaa at 71=(Ile or Thr); Xaa at res.
819 76= (Phe or Tyr); Xaa at res. 78 = (Asp, Glu or Ser);
820 Xaa at res. 80= (Ser or Asn); Xaa at res. 84 = (Ile or
821 Asp); Xaa at res. 85 Arg); Xaa at res. 87 = (Tyr, Ala
822 or His); and Xaa at res. 93=(Arg or Lys)

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824 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
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826 Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe
827 1 5 → 10 → 5 10
828 Xaa Asp Leu Gly Trp Xaa Asp Trp Xaa Ile
829 15 20
830 Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys
831 25 30
832 Glu Gly Cys Xaa Phe Pro Leu Xaa Ser Xaa
833 35 40
834 Met Asn Ala Thr Asn His Ala Ile Xaa Thr
835 45 50
836 Leu Xaa Xaa Xaa Xaa Xaa Xaa Val
837 55
838 Pro Lys Xaa Cys Cys Ala Pro Thr Xaa Leu
839 6065

space

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Xaa Ala Xaa Ser Val Leu Tyr Xaa Asp
70 75
Xaa Ser Xaa Asn Val Xaa Leu Xaa Lys
80 85
Xaa Pro Asn Met Val Val Xaa Ala Cys Gly
90 95
Cys His

- (2) INFORMATION FOR SEQ ID NO:6:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH:437 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE:no
(vi) ORIGINAL SOURCE:

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(A) ORGANISM: Human

(F) TISSUE TYPE: placenta

(ix) FEATURE:

(A) NAME: OP1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Space between nucleic acid & nucleic number

TCC ACG GGG
Ser Thr Gly
1
AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG 42
Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr
5 10
CCC AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC 75
Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn
15 20 25
GTG GCA GAG AAC AGC AGC AGC GAC CAG AGG CAG 108
Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln
30 35
GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC 141
Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe
40 45
CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG 174
Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala
50 55
CCT GAA GGC TAC GCC GCC TAC TAC TGT GAG GGG 207
Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly
60 65
GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG AAC 240
Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
70 75 80
GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC 273
Ala Thr Asn His Ala Ile Val Gln Thr Leu Val
85 90

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984 CAC TTC ATC AAC CCG GAA ACG GTG CCC AAG CCC 306
985 His Phe Ile Asn Pro Glu Thr Val Pro Lys Pro
986 95 100
987 TGC TGT GCG CCC ACG CAG CTC AAT GCC ATC TCC 339
988 Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser
989 105 110
990 GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC 372
991 Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
992 115 120
993 CTG AAG AAA TAC AGA AAC ATG GTG GTC CGG GCC 405
994 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala
995 125 130 135
996 TGT GGC TGC CAC TAGCTCCTCC GAGAATTCAG 437
997 Cys Gly Cys His
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1000 (2) INFORMATION FOR SEQ ID NO:7:
1001 (i) SEQUENCE CHARACTERISTICS:
1002 (A) LENGTH:102 amino acids
1003 (B) TYPE: amino acid
1004 (D) TOPOLOGY: linear
1005 (ii) MOLECULE TYPE: protein
1006 (ix) FEATURE:
1007 (D) OTHER INFORMATION:

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1008 wherein each Xaa independently represents one of
1009 the 20 naturally occurring L-isomer, α -amino acids.

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1011 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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1013 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1014 1 5 10

1015 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1016 15 20

1017 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa

1018 25 30

1019 Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa

1020 35 40

1021 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

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1054 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys

1055 60 65

1056 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1057 70 75

1058 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

1059 80 85

1060 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys

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1061 90 95
1062 Xaa Cys Xaa
1063 100
1064
1065 (2) INFORMATION FOR SEQ ID NO:8:
1066 (i) SEQUENCE CHARACTERISTICS:
1067 (A) LENGTH:97 amino acids
1068 (B) TYPE: amino acid
1069 (D) TOPOLOGY: linear
1070 (ii) MOLECULE TYPE: protein
1071 (ix) FEATURE:
1072 (D) OTHER INFORMATION:
1073 wherein each Xaa independently represents one of
1074 the 20 naturally occurring L-isomer, α -amino acids
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1076 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
1077
1078 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1079 1 5 10
1080 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1081 15 20
1082 Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
1083 25 30
1084 Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1085 35 40
1086 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1087 45 50 55
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1120 Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa
1121 60 65
1122 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1123 70 75
1124 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1125 80 85
1126 Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa
1127 90 95
1128
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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME: hOP-2P

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

1139
1140 Pro Leu Arg Arg ArgGln
1141 1 5
1142 Pro Lys Lys Ser Asn Glu Leu ProGln
1143 10 15
1144 Ala Asn Arg Leu Pro Gly Ile PheAsp
1145 20
1146 Asp Val Asn Gly Ser His Gly ArgGln
1147 25 30
1148 Val Cys Arg Arg His Glu Leu TyrVal
1149 35 40
1150 Ser Phe Gln Asp Leu Gly Trp LeuAsp
1151 45 50
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1184 Tyr Val Ile Ala Pro Gln Gly TyrSer
1185 55 60
1186 Ala Tyr Tyr Cys Glu Gly Glu CysSer
1187 65
1188 Phe Pro Leu Asp Ser Cys Met AsnAla
1189 70 75
1190 Thr Asn His Ala Ile Leu Gln SerLeu
1191 80 85
1192 Val His Leu Met Lys Pro Asn AlaVal
1193 90 95
1194 Pro Lys Ala Cys Cys Ala Pro ThrLys
1195 100105
1196 Leu Ser Ala Thr Ser Val Leu TyrTyr
1197 110
1198 Asp Glu Ser Asn Asn Val Ile LeuArg
1199 115 120
1200 Lys Ala Arg Asn Met Val Val LysAla
1201 125 130
1202 Cys Gly Cys His
1203 135
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1206 (2) INFORMATION FOR SEQ ID NO:10:

1207 (i) SEQUENCE CHARACTERISTICS:

1208 (A) LENGTH: 133 amino acids

1209 (B) TYPE: amino acid

1210 (D) TOPOLOGY: linear

1211 (ii) MOLECULE TYPE: protein

1212 (ix) FEATURE:

1213 (A) NAME: hOP-2R

1214 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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1216 Arg ArgGln

1217 1

1218 Pro Lys Lys Ser Asn Glu Leu ProGln

1219 5 10

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1251 Ala Asn Arg Leu Pro Gly Ile PheAsp
1252 15 20
1253 Asp Val Asn Gly Ser His Gly ArgGln
1254 25 30
1255 Val Cys Arg Arg His Glu Leu TyrVal
1256 35
1257 Ser Phe Gln Asp Leu Gly Trp LeuAsp
1258 40 45
1259 Tyr Val Ile Ala Pro Gln Gly TyrSer
1260 50 55
1261 Ala Tyr Tyr Cys Glu Gly Glu CysSer
1262 60 65
1263 Phe Pro Leu Asp Ser Cys Met AsnAla
1264 70 75
1265 Thr Asn His Ala Ile Leu Gln SerLeu
1266 80
1267 Val His Leu Met Lys Pro Asn AlaVal
1268 85 90
1269 Pro Lys Ala Cys Cys Ala Pro ThrLys
1270 95 100
1271 Leu Ser Ala Thr Ser Val Leu TyrTyr
1272 105 110

space

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1273 Asp Glu Ser Asn Asn Val Ile LeuArg
1274 115120
1275 Lys Ala Arg Asn Met Val Val LysAla
1276 125
1277 Cys Gly Cys His
1278 130
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1281 (2) INFORMATION FOR SEQ ID NO:11:

1282 (i) SEQUENCE CHARACTERISTICS:

1283 (A) LENGTH: 160 amino acids

1284 (B) TYPE: amino acid
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1315 (D) TOPOLOGY: linear

1316 (ii) MOLECULE TYPE: protein

1317 (ix) FEATURE:

1318 (A) NAME: hOP-2S

1319 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
1320

1321 Ser GlnGln

1322 1

1323 Pro Phe Val Val Thr Phe Phe ArgAla

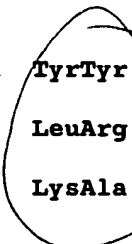
1324 5 10

1325 Ser Pro Ser Pro Ile Arg Thr ProArg

1326	15	20						
1327	Ala	Val	Arg	Pro	Leu	Arg	Arg	ArgGln
1328	25	30						
1329	Pro	Lys	Lys	Ser	Asn	Glu	Leu	ProGln
1330		35						
1331	Ala	Asn	Arg	Leu	Pro	Gly	Ile	PheAsp
1332	40	45						
1333	Asp	Val	Asn	Gly	Ser	His	Gly	ArgGln
1334		50		55				
1335	Val	Cys	Arg	Arg	His	Glu	Leu	TyrVal
1336	60	65						
1337	Ser	Phe	Gln	Asp	Leu	Gly	Trp	LeuAsp
1338	70	75						
1339	Tyr	Val	Ile	Ala	Pro	Gln	Gly	TyrSer
1340		80						
1341	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	CysSer
1342	85	90						
1343	Phe	Pro	Leu	Asp	Ser	Cys	Met	AsnAla
1344		95		100				
1345	Thr	Asn	His	Ala	Ile	Leu	Gln	SerLeu
1346	105	110						
1347	Val	His	Leu	Met	Lys	Pro	Asn	AlaVal
1348		115	120					
1349	Pro	Lys	Ala	Cys	Cys	Ala	Pro	ThrLys
1350	125							

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1382 Leu Ser Ala Thr Ser Val Leu TyrTyr
1383 130 135
1384 Asp Glu Ser Asn Asn Val Ile LeuArg
1385 140 145
1386 Lys Ala Arg Asn Met Val Val LysAla
1387 150 155
1388 Cys Gly Cys His
1389 160



LINE ERROR

ORIGINAL TEXT

24 Wrong application Serial Number
79 Wrong Amino Acid Designator
81 Wrong Amino Acid Designator
83 Wrong Amino Acid Designator
85 Wrong Amino Acid Designator
87 Wrong Amino Acid Designator
89 Wrong Amino Acid Designator
91 Wrong Amino Acid Designator
93 Wrong Amino Acid Designator
95 Wrong Amino Acid Designator
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101 Wrong Amino Acid Designator
103 Wrong Amino Acid Designator
135 Wrong Amino Acid Designator
137 Wrong Amino Acid Designator
77 Entered and Calc. Seq. Length differ
426 Wrong Amino Acid Designator
428 Wrong Amino Acid Designator
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424 Entered and Calc. Seq. Length differ
809 Response Exceeds Line Limitations
810 Response Exceeds Line Limitations
811 Response Exceeds Line Limitations
812 Response Exceeds Line Limitations
813 Response Exceeds Line Limitations
814 Response Exceeds Line Limitations
815 Response Exceeds Line Limitations
816 Response Exceeds Line Limitations
817 Response Exceeds Line Limitations
818 Response Exceeds Line Limitations
819 Response Exceeds Line Limitations
820 Response Exceeds Line Limitations
821 Response Exceeds Line Limitations
822 Response Exceeds Line Limitations
832 Wrong Amino Acid Designator
824 Entered and Calc. Seq. Length differ
923 Entered and Calc. Seq. Length differ
1140 Wrong Amino Acid Designator
1142 Wrong Amino Acid Designator

OK → (A) APPLICATION NUMBER: US 07/599,543
Ala Ala Arg Pro Leu Lys Arg ArgGlu
Pro Lys Lys Thr Asn Glu Leu ProHi
Pro Asn Lys Leu Pro Gly Ile PheAs
Asp Gly His Gly Ser Arg Gly ArgGlu
Val Cys Arg Arg His Glu Leu TyrVa
Arg Phe Arg Asp Leu Gly Trp LeuAs
Trp Val Ile Ala Pro Gln Gly TyrSe
Ala Tyr Tyr Cys Glu Gly Glu CysAl
Phe Pro Leu Asp Ser Cys Met AsnAl
Thr Asn His Ala Ile Leu Gln SerLe
Val His Leu Met Lys Pro Asp ValVa
Pro Lys Ala Cys Cys Ala Pro ThrLy
Leu Ser Ala Thr Ser Val Leu TyrTy
Asp Ser Ser Asn Asn Val Ile LeuAr
Lys His Arg Asn Met Val Val LysAl
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
Ala Val Arg Pro Leu Arg Arg ArgGlu
Pro Lys Lys Ser Asn Glu Leu ProGlu
Ala Asn Arg Leu Pro Gly Ile PheAs
Asp Val His Gly Ser His Gly ArgGlu
Val Cys Arg Arg His Glu Leu TyrVa
Ser Phe Gln Asp Leu Gly Trp LeuAs
Trp Val Ile Ala Pro Gln Gly TyrSe
Ala Tyr Tyr Cys Glu Gly Glu CysSe
Phe Pro Leu Asp Ser Cys Met AsnAl
Thr Asn His Ala Ile Leu Gln SerLe
Val His Leu Met Lys Pro Asn AlaVa
Pro Lys Ala Cys Cys Ala Pro ThrLy
Leu Ser Ala Thr Ser Val Leu TyrTy
Asp Ser Ser Asn Asn Val Ile LeuAr
Lys Ala Arg Asn Met Val Val LysAl
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
at res. 19 = (Ile or Val); Xaa at res.23
Xaa at res.26 = (Ala or Ser); Xaa at res
or Ser); Xaa at res.38= (Asn or Asp); Xa
(Tyr or Cys); Xaa at res.49 = (Val or Le
res.52= (His or Asn); Xaa at res. 53 = (
Leu); Xaa at res. 54 = (Ile or Met); Xaa
or Lys); Xaa at res. 56 = (Glu, Asp or A
57=(Thr, Ala or Val); Xaa at res. 61 = (
Xaa at res. 67=(gln or Lys); Xaa at res.
(Asn or Ser); Xaa at 71=(Ile or Thr); Xa
76= (Phe or Tyr); Xaa at res. 78 = (Asp,
Xaa at res. 80= (Ser or Asn); Xaa at res
Asp); Xaa at res. 85 Arg); Xaa at res. 8
or His); and Xaa at res. 93=(Arg or Lys)
Glu Gly Cys Xaa Phe Pro Leu XaaSer Xaa
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
Pro Leu Arg Arg ArgGlu
Pro Lys Lys Ser Asn Glu Leu ProGlu

LINE ERROR

ORIGINAL TEXT

1144 Wrong Amino Acid Designator
1146 Wrong Amino Acid Designator
1148 Wrong Amino Acid Designator
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1138 Entered and Calc. Seq. Length differ
1216 Wrong Amino Acid Designator
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1214 Entered and Calc. Seq. Length differ
1321 Wrong Amino Acid Designator
1323 Wrong Amino Acid Designator
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1349 Wrong Amino Acid Designator
1382 Wrong Amino Acid Designator
1384 Wrong Amino Acid Designator
1386 Wrong Amino Acid Designator
1319 Entered and Calc. Seq. Length differ

Ala	Asn	Arg	Leu	Pro	Gly	Ile	PheAs
Asp	Val	Asn	Gly	Ser	His	Gly	ArgGl
Val	Cys	Arg	Arg	His	Glu	Leu	TyrVa
Ser	Phe	Gln	Asp	Leu	Gly	Trp	LeuAs
Tyr	Val	Ile	Ala	Pro	Gln	Gly	TyrSe
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	CysSe
Phe	Pro	Leu	Asp	Ser	Cys	Met	AsnAl
Thr	Asn	His	Ala	Ile	Leu	Gln	SerLe
Val	His	Leu	Met	Lys	Pro	Asn	AlaVa
Pro	Lys	Ala	Cys	Cys	Ala	Pro	ThrLy
Leu	Ser	Ala	Thr	Ser	Val	Leu	TyrTy
Asp	Glu	Ser	Asn	Asn	Val	Ile	LeuAr
Lys	Ala	Arg	Asn	Met	Val	Val	LysAl
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:9:						
Arg	ArgGln						
Pro	Lys	Lys	Ser	Asn	Glu	Leu	ProGl
Ala	Asn	Arg	Leu	Pro	Gly	Ile	PheAs
Asp	Val	Asn	Gly	Ser	His	Gly	ArgGl
Val	Cys	Arg	Arg	His	Glu	Leu	TyrVa
Ser	Phe	Gln	Asp	Leu	Gly	Trp	LeuAs
Tyr	Val	Ile	Ala	Pro	Gln	Gly	TyrSe
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	CysSe
Phe	Pro	Leu	Asp	Ser	Cys	Met	AsnAl
Thr	Asn	His	Ala	Ile	Leu	Gln	SerLe
Val	His	Leu	Met	Lys	Pro	Asn	AlaVa
Pro	Lys	Ala	Cys	Cys	Ala	Pro	ThrLy
Leu	Ser	Ala	Thr	Ser	Val	Leu	TyrTy
Asp	Glu	Ser	Asn	Asn	Val	Ile	LeuAr
Lys	Ala	Arg	Asn	Met	Val	Val	LysAl
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:10:						
Ser	GlnGln						
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Ala	Val	Arg	Pro	Leu	Arg	Arg	ArgGl
Pro	Lys	Lys	Ser	Asn	Glu	Leu	ProGl
Ala	Asn	Arg	Leu	Pro	Gly	Ile	PheAs
Asp	Val	Asn	Gly	Ser	His	Gly	ArgGl
Val	Cys	Arg	Arg	His	Glu	Leu	TyrVa
Ser	Phe	Gln	Asp	Leu	Gly	Trp	LeuAs
Tyr	Val	Ile	Ala	Pro	Gln	Gly	TyrSe
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	CysSe
Phe	Pro	Leu	Asp	Ser	Cys	Met	AsnAl
Thr	Asn	His	Ala	Ile	Leu	Gln	SerLe
Val	His	Leu	Met	Lys	Pro	Asn	AlaVa
Pro	Lys	Ala	Cys	Cys	Ala	Pro	ThrLy
Leu	Ser	Ala	Thr	Ser	Val	Leu	TyrTy
Asp	Glu	Ser	Asn	Asn	Val	Ile	LeuAr
Lys	Ala	Arg	Asn	Met	Val	Val	LysAl
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:11:						

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/599,543C

DATE: 10/01/91
TIME: 14:53:57

MANDATORY IDENTIFIER THAT WAS NOT FOUND

LINE ORIGINAL TEXT

CORRECTED TEXT

76 (A) NAME: mOP2 (mature)
155 (A) NAME: mOP2
423 (A) NAME: hOP2 (mature)
535 (A) NAME: hOP2
922 (A) NAME: OP1
1137 (A) NAME: hOP-2P
1213 (A) NAME: hOP-2R
1318 (A) NAME: hOP-2S

(A) NAME/KEY: mOP2 (mature)
(A) NAME/KEY: mOP2
(A) NAME/KEY: hOP2 (mature)
(A) NAME/KEY: hOP2
(A) NAME/KEY: OP1
(A) NAME/KEY: hOP-2P
(A) NAME/KEY: hOP-2R
(A) NAME/KEY: hOP-2S